

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2002, 21:43:19 ; Search time 2351.15 Seconds

(without alignments)  
168.399 Million cell updates/sec

Title: US-09-851-670-2

Perfect score: 24  
Sequence: 1 cgacaataatgaaaaaacagctgcgc 24

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 586436

Minimum DB seq length: 0  
Maximum DB seq length: 60

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

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35: em\_htg\_rnd: \*  
36: em\_htg\_other: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.6	60.8	42	6 121514	121514 Sequence 61
2	14.6	60.8	58	6 A42718	A42718 Sequence 50
3	14.6	60.8	58	6 187224	187224 Sequence 50
4	14.4	60.0	51	6 AX161485	AX161485 Sequence
5	14.2	59.2	42	6 E31994	E31994 Process for
6	14.2	59.2	57	9 HUMACTGAM	K00791 human fibro
7	13.8	57.5	21	6 AX166770	AX166770 Sequence
8	13.8	57.5	32	6 AX044019	AX044019 Sequence
9	13.6	56.7	20	12 AB068316	AB068316 Synthetic
10	13.4	55.8	20	6 AR082336	AR082336 Sequence
11	13.4	55.8	20	6 AR120878	AR120878 Sequence
12	13.4	55.8	20	6 178382	178382 Sequence 18
13	13.4	55.8	37	6 A46389	A46389 Sequence 11
14	13.4	55.8	37	6 AR078965	AR078965 Sequence
15	13.4	55.8	47	6 AX040147	AX040147 Sequence
16	13.4	55.8	51	9 HSCD85701	Z50814 H. sapiens m
17	13.2	55.0	21	6 AB6494	AB6494 Sequence 1
18	13.2	55.0	31	6 177112	177112 Sequence 9
19	13.2	55.0	51	6 AX160359	AX160359 Sequence
20	13	54.2	28	6 AX028853	AX028853 Sequence
21	13	54.2	36	6 A21615	A21615 Oligonucleo
22	13	54.2	45	6 E12626	E12626 PCR primer
23	13	54.2	45	6 E13645	E13645 Primer. 6/1
24	12.8	53.3	30	6 AR028165	AR028165 Sequence
25	12.8	53.3	30	6 AR138695	AR138695 Sequence
26	12.8	53.3	44	6 AX008704	AX008704 Sequence
27	12.8	53.3	46	6 AX008705	AX008705 Sequence
28	12.8	53.3	50	6 AX160360	AX160360 Sequence
29	12.8	53.3	51	6 AX157377	AX157377 Sequence
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31	12.8	53.3	51	6 AX160873	AX160873 Sequence
32	12.8	53.3	51	6 AX160874	AX160874 Sequence
33	12.8	53.3	51	6 AX160948	AX160948 Sequence
34	12.8	53.3	51	6 AX161486	AX161486 Sequence
35	12.6	52.5	23	6 AR102864	AR102864 Sequence
36	12.6	52.5	23	6 AR129408	AR129408 Sequence
37	12.6	52.5	24	6 136855	136855 Sequence 3
38	12.6	52.5	29	6 E03251	E03251 Synthetic o
39	12.6	52.5	32	6 AR110345	AR110345 Sequence
40	12.6	52.5	42	6 AX166900	AX166900 Sequence
41	12.6	52.5	44	6 A33239	A33239 Synthetic P
42	12.6	52.5	51	6 AX160664	AX160664 Sequence
43	12.4	51.7	20	6 AR157104	AR157104 Sequence
44	12.4	51.7	25	6 AX116636	AX116636 Sequence
45	12.4	51.7	26	6 AX035589	AX035589 Sequence

## ALIGNMENTS

RESULT	1				
LOCUS	121514	Sequence 61	42 bp	DNA	PAT
DEFINITION	121514	Sequence 61 from patent US 5521300.			07-OCT-1996
ACCESSION	121514				
VERSION	121514.1	GI:1601868			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 42)				
AUTHORS	Shah, J.S., Nietupski, R.M. and Liu, J.				
TITLE	Oligonucleotides complementary to mycobacterial nucleic acids				
JOURNAL	Patent: US 5521300-A 61 28-MAY-1996;				
FEATURES	Location/Qualifiers				
Source	1..42				
BASE COUNT	13 a 14 c 9 g 6 t				
ORIGIN					

Query Match	60.88;	Score 14.6;	DB 6;	Length 58,
Best Local Similarity	81.08;	Pred. No. 6.9e+03;		

PI HISASHI YASUE, YOSHIO KAWARA, SHINICHI SUGIMOTO PC  
C12N5/09, C12M1/21, C12N9/12//((C12N15/09, C12R1:125), (C12N1/21, PC  
C12R1:19), (C12N9/12, C12R1:19), C12N5/00, (C12M1/25) CC  
PC (C12N9/12, C12R1:19), C12N5/00, (C12M1/25) CC  
FH Location/Qualifiers  
FH Key  
FT 1..42  
FT source  
FT /organism='Artificial Sequence'.

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  14 a 7 c 9 g 12 t
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Best Local Similarity 84.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 aatggaaaacagctgcg 23
    ||||| ||||| ||
Db 12 AATGGAAATACAGCTGC 30

RESULT 6
HUMACTGM 57 bp mRNA PRI 30-OCT-1994
DEFINITION human fibroblast gamma-actin mRNA, 5' end.
ACCESSION K00791
VERSION K00791.1 GI:178046
KEYWORDS actin; gamma-actin.
SOURCE human fibroblast (simian virus 40-transformed) cDNA to mRNA, clone
          phf-gamma-a-1.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
          1 (bases 1 to 57)
REFERENCE Gunning, P., Ponte, P., Okayama, H., Engel, J., Biau, H. and Kedes, L.,
          isolation and characterization of full-length cDNA clones for human
          alpha-, beta-, and gamma-actin mRNAs: skeletal but not cytoplasmic
          actins have an amino-terminal cysteine that is subsequently removed
          Mol. Cell. Biol. 3 (5), 787-795 (1983)
JOURNAL MEDLINE 83244575
COMMENT [1] also sequenced alpha- and beta-actin mRNAs.
          mature actin has an acidic amino terminus. with alpha-actin, the
          initial translation product has a met-cys preceding this acidic
          amino acid; however, beta- and gamma-actin have only a met
          preceding [1].

FEATURES
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  gene
    7. 57
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  CDS
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    /codon_start=1
    /db_xref="GDB:G00-120-536"
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    /translation="MEEEIALVLDNGSGMC"
    10. >57
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Best Local Similarity 84.2%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 aatggaaaacagctgcg 24
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Db 6 AATGGAAAGAGATGCC 24

RESULT 7

AX166770
LOCUS AX166770 21 bp DNA PAT 22-JUN-2001
DEFINITION Sequence 261 from Patent WO0138503.
ACCESSION AX166770
VERSION AX166770.1 GI:14547045
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
          1 (bases 1 to 21)
REFERENCE Plowman, G.D., Whyte, D., Manning, G.S., Sudarsanam, S.S., Martinez, R.,
          Flanagan, P. and Clary, D.S.
          Novel human protein kinases and protein kinase-like enzymes
          Patent: WO 0138503-A 261 31-MAY-2001;
          Sugen, Inc. (US)
TITLE
JOURNAL
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BASE COUNT
  6 a 6 c 4 g 5 t
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Query Match
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Best Local Similarity 88.2%; Pred. No. 1.4e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 tggaaaacagctgcg 24
    ||||| ||||| ||
Db 5 TCCAAAACAGCTGCC 21

RESULT 8
AX044019 32 bp DNA PAT 24-NOV-2000
LOCUS AX044019
DEFINITION Sequence 98 from Patent WO0066791.
ACCESSION AX044019
VERSION AX044019.1 GI:11342903
KEYWORDS
SOURCE Neisseria meningitidis.
          Neisseria meningitidis
          Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
          Neisseria.
          1 (bases 1 to 32)
REFERENCE Pizze, M., Hickey, E., Peterson, J., Rettelin, H., Venter, J.C.,
          Masignani, V., Galeotti, C., Mora, M., Ratti, G., Scarselli, M.,
          Scarlato, V., Rappunoli, R., Frazer, C.M. and Grandi, G.
          Neisseria genomic sequences and methods of their use
          Patent: WO 0066791-A 98 09-NOV-2000;
          CHIRON CORPORATION (US); THE INSTITUTE FOR GENOMIC RESEARCH (US)
TITLE
JOURNAL
FEATURES
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    1. 32
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BASE COUNT
  10 a 9 c 6 g 7 t
ORIGIN

Query Match
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Best Local Similarity 88.2%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 caaatgaaaacagct 20
    ||||| ||||| |||||
Db 10 CATATGGAACACAGCT 26

RESULT 9
AB068316 20 bp DNA SYN 08-AUG-2001
LOCUS AB068316
DEFINITION Synthetic construct DNA, forward primer for human SRS sts-wt-19810
          at 1p36.

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ACCESSION   AB068316
VERSION     AB068316.1  GI:15129120
KEYWORDS
SOURCE      synthetic construct DNA.
ORGANISM    synthetic construct
            artificial sequence.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Chen, Y. Z., Hayashi, Y., Wu, J. G., Takaoka, E., Maekawa, K.,
            Matsunabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H.,
            Morohashi, A., Ohita, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A.,
            and Soeda, E.
TITLE       A bac-based sts-content map spanning a 35-mb region of human
            chromosome 1p35-p36
JOURNAL     Genomics 74 (1), 55-70 (2001)
MEDLINE    21269192
REFERENCE   2 (bases 1 to 20)
AUTHORS     Horii, A.
TITLE       Direct Submission
JOURNAL     Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
            Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES
            Location/Qualifiers
            source          1..20
                           /organism="synthetic construct"
                           /db_xref="taxon:32630"
            misc_feature    1..20
                           /note="forward primer for human STS sts-WI-19810 at 1p36
                           sts-WI-19810 obtained from clones B335616, B338N10,
                           B173013, B249C6, B281E22, B417D2, B452E22, B620C9, B690E2,
                           B4A4, Human BAC library RPCI-11"
BASE COUNT      8 a          6 c          3 g          3 t
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ORGANISM      unidentified
REFERENCE      unclassified.
AUTHORS        1 (bases 1 to 37)
TITLE          Kerry-Williams,S.M. and Gilbert,S.C.
JOURNAL        YEAST STRAINS AND MODIFIED ALBUMINS
                Patent: WO 9523857-A 11 08-SEP-1995;
                DELTA BIOTECHNOLOGY LTD (GB)
COMMENT        Other publication AU 1818395 950918.
FEATURES
SOURCE         1. .37
                /organism="unidentified"
                /db_xref="taxon:32644"
BASE COUNT     5 a      5 c      9 g      18 t
ORIGIN

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Best Local Similarity 55.8%; Score 13.4; DB 6; Length 37;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 gacaaatggaagaacagctgcc 24
    ||||| ||||| |||||
Db 34 GACAAACCAAAATAAGTCGCAC 12

RESULT 14
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LOCUS
DEFINITION    Sequence 11 from patent US 5965386.
ACCESSION     AR078965
VERSION       AR078965.1 GI:10005711
KEYWORDS
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 37)
AUTHORS       Kerry-Williams,S.Martin and Gilbert,S.Catherine.
TITLE         Yeast strains and modified albumins
JOURNAL       Patent: US 5965386-A 11 12-OCT-1999;
FEATURES
SOURCE        1. .37
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BASE COUNT    5 a      5 c      9 g      18 t
ORIGIN

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QY 2 gacaaatggaagaacagctgcc 24
    ||||| ||||| |||||
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RESULT 15
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LOCUS
DEFINITION    Sequence 43 from Patent WO0063438.
ACCESSION     AX040147
VERSION       AX040147.1 GI:11230097
KEYWORDS
SOURCE        human.
ORGANISM      Homo sapiens
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS       1 (bases 1 to 47)
TITLE         Gould-Rothberg,B.E. and Rastelli,L.
JOURNAL       Method of classifying a thyroid carcinoma using differential gene
                expression
                Patent: WO 0063438-A 43 26-OCT-2000;
                Curagen Corporation (US)
FEATURES
                Location/Qualifiers

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ORIGIN

Query Match
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Search completed: March 9, 2002, 00:48:33
Job time: 11114 sec

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